

	20	30	40	50		
1	MASTTPITME	DLQKALEAQ	RALRAGLAAG	ASQSRRPRPP	RHARLQHLPE	50
60	70	80	90	100		
51	MTPAVTPPEGP	APPRTGAMQR	KDWSRAPPPP	SERQESRSQT	<u>PAPKPSRAPP</u>	100
110	120	130	140	150		
101	<u>OOPOPPRMOT</u>	GRGGSAPRPE	LCPPPTNPFOA	AVARGLRPPL	HOPOTEAPTE	150
160	170	180	190	200		
151	ACVTSMWSE	GEGAVFYRVD	LHFINLGTTP	LOEDGRMOPA	LHYNPCGPEP	200
210	220	230	240	250		
201	PAHVVRAYNQ	PAGOVRGVNG	KCERTYAEQD	FRVGGTRYHHR	LLRMPVRGLD	250
260	270	280	290	300		
251	GOTAPLPPHT	TERIETRSAR	HPWRIRFGAP	CAFLAGLLA	AVAVGATARAG	300
310	320	330	340	350		
301	LQPRADMAAP	<u>PMPPQPPRAH</u>	GOHYCHHHHQ	LPFLGHGHH	GGTLRVCQHH	350
360	370	380	390	400		
351	RNASOVLPGH	WLQGGNGCYN	LSDWHQGTHV	CHTKHMDFWC	VEHDRPPPAT	400
410	420	430	440	450		
401	PTSLTTAANY	IAAAATPATAP	PPCHAGLND	CGGFLSGCGP	MRLPTALTPG	450
460	470	480	490	500		
451	AVGDLRAVHH	RPVPAYPVCC	AMRWGLPPWE	LVILTARPED	GNTCRGVPAH	500
510	520	530	540	550		
501	PGTRCPPELYS	PMGRATCSPA	SALWLATANA	LSLDHAAAF	VLLVPMVLIF	550
560	570	580	590	600		
551	MVCRRACRRP	APPPPSPQSS	CRGTTPPAYG	EEAFTYLCTA	PGCATOTPVP	600
610	620	630	640	650		
601	VRLAGVGFES	KIVDGGCFAP	MOLEATGACI	CEIPTDVSCE	GLGAMVPTAP	650
660	670	680	690	700		
651	CARIWNGTOR	ACTFWAVNAY	SSGGYAOLAS	YFNPGGSYYK	OYHPTACEVE	700
710	720	730	740	750		
701	PAFGHSDAAC	WGFPTDTVMS	VFALASYVOH	PHKTVRVKFH	TETRTVWOLS	750
760	770	780	790	800		
751	VAGVSCNVT	EHPFCNTPHG	QLEVQVPPDP	COLVEYIMNY	TGNQQSRRG	800
810	820	830	840	850		
801	GSPNCHGPDM	ASPVQCQRHSP	DCSRLVGATP	ERPRRLRLVDA	DDPLLLRTAPG	850
860	870	880	890	900		
851	PGEVWVTPVI	GSQARKCGLH	IRAGPYGHAT	YEMPEWIHAA	TTSDPWHPPG	900
910	920	930	940	950		
901	PLGLKFKTVR	PVALPRALAP	PRNVRVTGCY	QCCTPALYEG	LAPGGGNCHL	950
960	970	980	990	1000		
951	TVNGEDVGAF	PPGKFVTAAL	LNTPPPYQVS	CGGESDRASA	GH.....	1000

FIGURE 1

5 10 15 20 25 30
 1 M A S T T P I M E D L Q K A L E A Q S R A A E L A A G
 5 I A S Q S R R P P P R Q R D S S T S G D O S G R D S G G P R
 9 I R R R G N R G R G Q R D O W S R A P P P P E E R Q E S R S
 13 I T P P P P P P S R A P P Q Q P Q P P R M Q T G R G G S A P R P
 121 E L G P P T N P F Q A A V A R G L R P P L H D P D T E A P T
 151 E A C V T S H L W S E G Q G A V F Y R V D L H F T N L G T P
 181 P L D E D G R W D P A L M Y N P C G P E P P A H V V R A Y N
 211 Q P A G D V R G V W G K G E R T Y A E Q D F R V G G T R W H
 241 R L L R M P V R G L D G D S A P L P P H T T E R I E T R S A
 271 R H P W R I R F G A P Q A F L A G L L A T V A V G T A R A
 301 G L Q P R A D M A A P P T L P Q P P R ^{CUS} H G Q H Y G H H H H
 331 Q L P F L G H D G H H G G T L R V G Q H Y R N A S D V L P G
 361 H W L Q G G W G C Y N L S D W H Q G T H V C H T K H M D E W
 391 C V E H A R P P P A T P T P L T T A A N S T T A A T P A T A
 421 P A P C H A G L N D S C G G F L S G C G P M R L R H G A D T
 451 R C G R L I C G L S T T A Q Y P P T R F G C A M R W G L P P
 481 W E L V V L T A R P E D G W T C R G V P A H P G A R C P E L
 511 V S P M G R A T C S P A S A L W L A T A N A L S L D H A L A
 541 A F V L S V P W V L I F M V C R R A C R R R G A A A A L T A
 571 V V L Q G Y N P P A Y G E E A F T Y L C T A P G C A T Q A P
 601 V P V R L A G V R F E S K I V O G G C F A P W D L E A T G A
 631 C I C E I P T D V S C E G L G A W V P A A P C A R I W N G T
 661 Q R A C T F W A V N A Y S S G G Y A Q L A S Y F N P G G S Y
 691 Y K Q Y H P T A C E V E P A F G H S D A A C W G F P T D T V
 721 M S V F A L A S Y Y Q H P H K T V R V K F H T E T R T V W Q
 751 L S V A G V S C H V T T E H P F C N T P H G Q L E V Q V P P
 781 D P G D L V E Y I M N Y T G N Q Q S R W G L G S P N C H G P
 811 D W A S P V C Q R H S P D C S R L V G A T P E R P R L R L V
 841 D A D D P L L R T A P G P G E V W V T P V I G S Q A R K C G
 871 L H I R A G P Y G H A T V E M P E W I H A H T T S D P W H P
 901 P G P L G L K F K T V R P V A L P R T L A P P R N V R V T G
 931 C Y Q C G T P A L V E G L A P G G G N C H L T V N G E D V G
 961 A V P P G K F V T A A L L N T P P P Y Q V S C G G E S D R A
 991 S A R V I D P A A Q S F T G V V Y G T H T T A V S E T R Q T
 1021 W A E W A A A H W W Q L T L G A T C A L P L A G L L A C C A
 1051 K C L Y Y L R G A I A P R

FIGURE 2

5 10 15 20 25 30
1 M A S T T P I T M E D L Q K A L E A Q S R A L R A E L A A G
31 A S Q S R R P R P P R Q R D S S T S G D D S G R D S G G P R
61 R R R G N R G R G Q R R D W S R A P P P P E E R Q E S R S
91 T P A P P T R E R A P P Q Q P Q P P R M Q T G R G G S A P R P
121 E L G P P T N P F Q A A V A R G L R P P L H O P D T E A P T
151 E A C V T S W L W S E G Q G A V F Y R V D L H F T N L G T P
181 P L D E O G R W D O P A L M Y N P C G P E P P A H V V R A Y N
211 Q P A G D V R G V W G K G E R T Y A E Q D F R V G G T R W H
241 R L L R M P V R G L D G D S A P L P P H T T E R I E T R S A
271 R H P W R I R F G A P Q A F L A G L L L A T V A V G T A R A
301 G L Q P R A O M A A P P T E P Q P P ^C A H G Q H Y G H H H H
- 331 Q L P F L G H D G H H G G T E R V G Q H Y R N A S D V L P G
361 H W L Q G G W G C Y N L S D W H Q G T H V C H T K H M D F W
391 C V E H A R P P P A T P T P L T T A A N S T T A A T P A T A
421 P A P C H A G L N D S C G G F L S G C G P M R L R H G A D T
451 R C G R L I C G L S T T A Q Y P P T R F G C A M R W G L P P
481 W E L V V L T A R P E D G W T C R G V P A H P G A R C P E L
511 V S P M G R A T C S P A S A L W L A T A H A L S L D H A L A
541 A F V L S V P W V L I F M V C R R A C R R R G A A A A L T A
571 V V L Q G Y N P P A Y G E E A F T Y L C T A P G C A T Q A P
601 V P V R L A G V R F E S K I V D G G C F A P W D L E A T G A
631 C I C E I P T D V S C E G L G A W V P A A P C A R I W N G T
661 Q R A C T F W A V N A Y S S G G Y A Q L A S Y F N P G G S Y
691 Y K Q Y H P T A C E V E P A F G H S D A A C W G F P T O T V
721 M S V F A L A S Y V Q H P H K T V R V K F H T E T R T V W Q
751 L S V A G V S C N V T T E H P F C N T P H G Q L E V Q V P P
781 D P G D L V E Y I M N Y T G N Q Q S R W G L G S P N C H G P
811 D W A S P V C Q R H S P D C S R L V G A T P E R P R L R L V
841 D A D D P L L R T A P G P G E V W V T P V I G S Q A R K C G
871 L H I R A G P Y G H A T V E M P E W I H A H T T S D P W H P
901 P G P L G L K F K T V R P V A L P R T L A P P R N V R V T G
931 C Y Q C G T P A L V E G L A P G G G N C H L T V N G E D V G
961 A V P P G K F V T A A L L N T P P P Y Q V S C G G E S D R A
991 S A R V I D P A A Q S F T G V V Y G T H T T A V S E T R Q T
1021 W A E W A A A H W W Q L T L G A T C A L P L A G L L A C C A
1051 K C L Y Y L R G A I A P R

FIGURE 2

10	20	30	40	50	
1 MGARASVLSG	GELDRWEKIR	LRPGGKKYK	LKHIVMASRE	LERFAVNPG	50
60	70	80	90	100	
51 LETSEGCROI	LGQLQPSLQT	GSEELRSLYN	TVATLYCVHQ	RIEIKDTKEA	100
110	120	130	140	150	
101 LDKIEEEQNK	SKKKAQQAAA	DTGHSSQVSQ	NYPIVQNIQG	QMVHQAI	150
160	170	180	190	200	
151 TLNAWVKVE	EKAFSPEVIP	MFSALSEGAT	PQDLNTMLNT	VGGHQAAQM	200
210	220	230	240	250	
201 LKETINEEAA	EWORVHPVHA	GPIAPGQMRE	PRGSDIAGTT	STLQEIQIGWM	250
260	270	280	290	300	
251 TNNPPPIPVG	EYKRMWILGL	NKIVRMYSPT	SI	DIRQGPK	300
310	320	330	340	350	
301 YKTLRAEQAS	QEYKNWMTET	LLVQMANPDC	KTILKALGP	ATLEEMMTAC	350
360	370	380	390	400	
351 QGVGGPGHKA	RVLAEAMSQV	TNTATIMMQR	GNFRNQRKMW	KCFNCGKEGH	400
410	420	430	440	450	
401 TARNCRAPRK	KGCRKCGKEG	HQMKDCTERQ	ANFLGKICLP	TREGQQGIFR	450
460	470	480	490	500	
451 ADQSQQPHHF	FRADQSQQPH	QKRASGLG			500

FIGURE 3

	20	30	40	50		
1	MRVKEKYOHL	WRWGWKGTM	LLCILMICSA	TEKLHWTYYY	GVPVWKEATT	50
	60	70	80	90	100	
51	TLFCASAKA	YOTEVHNWVA	THACVPTDPN	POEVVLVNVT	ENFNMMWKNDM	100
	110	120	130	140	150	
101	VEQMHEOIIIS	LWDQSLKPCV	KLTPLCVSLK	CTDGNATNT	NSSNTNSSSG	150
	160	170	180	190	200	
151	EHMMMEKGEIK	NCSFNISTSI	RCKVQKEYAF	FYKLDIIPID	NOTTSYTLTS	200
	210	220	230	240	250	
201	CHTSVITQAC	PKVSFEPPIPI	HYCAPAGFAI	LKCNNKTFNG	TCPCTNVSTV	250
	260	270	280	290	300	
251	QCTHGIRPVV	STQLLLNGSL	AAEEVIRSA	NFTDNAKTII	VQLNQSVEIN	300
	310	320	330	340	350	
301	CTRPNNNTRK	SIRIQRGPCR	AFVTICKIGN	MROAHCNISR	AKWNATLKQI	350
	360	370	380	390	400	
351	ASKLREQFGN	NKTIIFKQSS	GGDPEIVTHS	FNCGGEFFYC	NSTQLFNSTW	400
	410	420	430	440	450	
401	FNSTWSTECS	NNTEGSDTIT	LPCRIKQFIN	MWQEVGKAMY	APPISGQIRC	450
	460	470	480	490	500	
451	SSNITGLLLT	RDGGNNNNNGS	EIFRPGGGDM	RONWRSELYK	YKVVKIEPLG	500
	510	520	530	540	550	
501	VAPTKAKRRV	VQREKRAVGI	GALFLGFLGA	AGSTMGARSM	TLTVQARQLL	550
	560	570	580	590	600	
551	SGIVQQQNNL	LRAIEAQQHL	LQLTVWGIKQ	LQARILAVER	YLKDQQQLGI	600
	610	620	630	640	650	
601	WGCSGKLICT	TAVPWNASHS	NKSLEQIMNN	MTWMEWOREI	NNYTSLIHSL	650
	660	670	680	690	700	
651	IEESQNQQEK	NEOBELLELDK	WASLWNNWFNI	THWLWYIKIF	IMIVGGLVGL	700
	710	720	730	740	750	
701	RIVFAVLSIV	NRVRQGYSPL	SFQTHLPTPR	GPDRPEGIEE	EGGERDRDRS	750
	760	770	780	790	800	
751	IRLVNGSLAL	IWODLRSLCL	FSYHRLROLL	LIVTRIVELL	GRRGWEALKY	800
	810	820	830	840	850	
801	WWNLLQYNSQ	ELKNSAVSLL	NATAIAVAEG	TDRVIEVVQG	ACRAIRHIPR	850
	860	870	880	890	900	
851	RIRQGLERIL	L				900

FIGURE 4

10	20	30	40	50
1 MKTTLKMTAL	AALSAFVLAG	CGSHOMKSEE	HANMQLQQQA	VLGLNMMQDS
60	70	80	90	100
51	GEYKALAYQA	YNAAKVAFDH	AKVAKGKKKA	VVADLDETM
101	<u>QNNKPFDGKO</u>	<u>NTRWVNDARQS</u>	<u>RAVPGAVEFN</u>	<u>NYVNSHNGKV</u>
160	170	180	190	200
151	EKSGTIODMK	RLGFNGVEES	AFYLUKKOKSA	KAARFAEIEK
210	220	230	240	250
201	ONLDOFGNTV	YGKLNADRRRA	FVDONQGKFG	KTFIMLPNAN
260	270	280	290	300
251	GYFKKDTQGQ	IKARLOAVQA	WOGK	

FIGURE 5

	10	20	30	40	50	
1	<u>I</u> QPPKNLLFS	SLLFSSLLFS	SAAQAASEDR	RSPYYYQADL	AYAAERITHD	50
	60	70	80	90	100	
51	YPQATGANNT	STVSDYFRNI	RAHSIHPRVS	VGYDFGGWRI	AADYASYRKW	100
	110	120	130	140	150	
101	NNNKYSVNTK	ELENKHNNKK	DLKTENQENG	TFHAASSLGL	SAIYDFKLKG	150
	160	170	180	190	200	
151	KFKPYICARV	AYGHVRHSID				200

FIGURE 6

10 20 30 40 50

7 FVTKM*YKTL OKYLRRRLIL NISIV*K*LS EKR*I*MNKK KMIILTSLASV 56

60 70 80 90 100

57 AILGAGFVAS QPTVVRAEES PVASQSKAEK DYDAAKKODAK NAKKAVEDAQ 106

110 120 130 140 150

107 KALDDAKAAQ KKYDDEDQKKT EEEKAALEKAA SEEMDKAVAA VQQAYLAYQQ 156

160 170 180 190 200

157 ATOKAAKDAA OKMIDEAKKR EEEAKTKFNT VRAMVPEPE QLAETKKSE 206

210 220 230 240 250

207 EAKQKAPELT KKLEEAKAKL EEAEKKATEA KQKVDAEEVA PQAKIAELEN 256

260 270 280 290 300

257 QVHRLEQELK EIDESESEDY AKEGFRAPLQ SKLDAAKAKL SKLEELSDKI 306

310 320 330 340 350

307 DELDAEIAKL EDOLKAAEEN NNVEDYFKEG LEKTIAAKKA ELEKTEADLK 356

360 370 380 390 400

357 KAVNEPEKPA PAPETPAPEA PAEQPKPAPA PQPAPAPKPE KPAEQPKPE 406

410 420 430 440 450

407 TDDQQAEEDY ARRSEEEYNR LTQQQPPKAE KPAPAPKTGW KQENGMMFY 456

460 470 480 490 500

457 NTGSMATGW LQNGSMYYL NSNGAMATGW LQYNGSMYYL NANGAMATGW 506

510 520 530 540 550

507 AKVNGSMYYL NANGAMATGW LQYNGSMYYL NANGAMATGW AKVNGSMYYL 556

560 570 580 590 600

557 NANGAMATGW LOYNGSMYYL NANGAMATGW AKVNGSMYYL NANGAMATGW 606

610 620 630 640 650

607 VKDGDOTHYYL EASGAMKASQ WFKVSDKHWY VNGLGALAVN TTVDGYKVNA 656

660 670 680 690 700

657 NGEWV*AO*I KAC*EHLTF* F*NKDKVRLN RFMFVFFRY. 706

10	20	30	40	50	
1 MNMKKATIAA	TAGIAVTAFR	APTIERSASTV	VVEAGDTLWG	IAQSKGTTVO	50
60	70	80	90	100	
51 AIKKANNLTT	DKIVPGQKLQ	VNNEVAAAEEK	TEKSVSATWL	NVRSGAGVN	100
110	120	130	140	150	
101 SIITSIKGGT	KVTVETTESN	GWHKITYNDG	KTGFVNGKYL	TDKAVSTPVA	150
160	170	180	190	200	
151 PTQEVKKETT	TQQAAPAAET	KTEVKQTTQA	<u>TTTPAPKVAET</u>	KETPVVDDQNA	200
210	220	230	240	250	
201 TTHAVKSGDT	IWALSVKYGV	SVQDIMSWNN	LSSSSIIYVGQ	<u>KLAIKQTANT</u>	250
260	270	280	290	300	
251 ATPKAEVKTE	APAAEKQAAP	VVKENTNTNT	ATTEKKETAT	<u>QQQTAPKAPT</u>	300
310	320	330	340	350	
301 EAAPAPAPS	TNTNANKTNT	NTNTNTNTNN	TNTNTPSKNT	NTNSNTNTNT	350
360	370	380	390	400	
351 NSHTNANQGS	SNNSNSSSAS	AIIAEAQKHL	CKAYSWGGNG	PTTFDCSGYT	400
410	420	430	440	450	
401 KYVFAKAGIS	LPRTSGAQYA	STTRISESQA	KPGDLVFFDY	GSGISHVGIY	450
460	470	480	490	500	
451 VGNGQMINAQ	DNGVKYDNIH	GSGWGKYLVG	FGRV.....	500

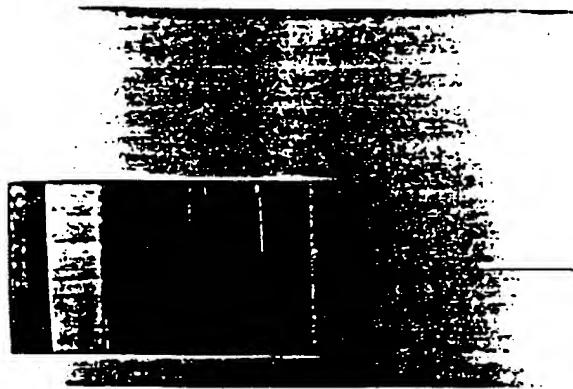
FIGURE 8

10 20 30 40 50
1 MKVSAALLCL LIAATFIPO GLAQPOAINA PVTCCYNFTN RKISVQRLAS 50
60 70 80 90 100
51 YRRITSSKCP KEAVIFKTIV AKEICADPKQ KMVQDSMDHL OKQTQTPKT. 100

FIGURE 9

10 20 30 40 50
1 KSTTCCYRFI NKKIPKORLE SYRRTTSSHC PREAVIFKDK EICADPTOKW 50
60 70 80 90 100
51 VQDFMKHLOK KTQTPKL 100

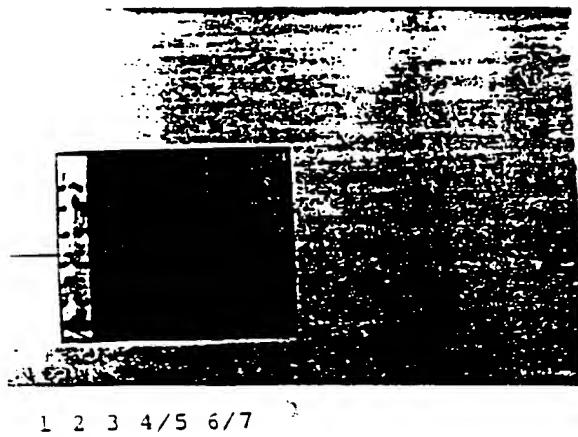
FIGURE 10



1 2/3 4/5/6 7/8 9/10

Immunoblots of RV antigens reacted with Mab's RV1, RV2, RV3 and RV4. RV antigen: strain MPV-77 (lot# 50678, Catalogue # EL-05-04) cultured in Vero cells. Purchased from Microsik Biosystems Inc., Toronto, Ontario. All Mab used as tissue culture fluid diluted 1/300. Lane 1 - Molecular weight markers of 97, 66, 45, 31, 21, and 14kD. Lane 1/3 - RV4; lane 4-5/6 - RV3; lane 7/8 - RV2; lane 9-10 - RV1. Lanes 1-9 all illustrate two proteins. 31 kD major and 45 kD minor, identified by reaction with Mab's 1-4.

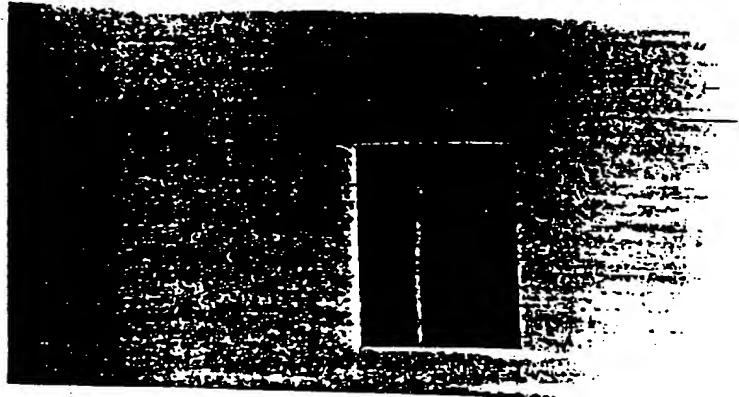
FIGURE 11



1 2 3 4/5 6/7

Immunoblots of bacterial antigens reacted with RV Mab RV1.
H. Influenzae b antigen from ATCC (#10211); *L. monocytogenes* from ATCC (#7644); *S. pneumoniae* from the Caribbean Regional Epidemiology Centre, CAREC, Trinidad; *N. meningitidis* A from ATCC #13077.
 Lane 1 - Molecular weight markers of 97, 66, 45, 31, 21, and 14 kD.
 Lane 2 - *H. Influenzae* b - proteins of approximate weights of 50, 45, 40, and 25 kD.
 Lane 3 - *L. monocytogenes* - proteins of approximate weights of 40 kD (major) and 66 kD (minor).
 Lane 4/5 - *S. pneumoniae* - proteins of approximate weights of 60 kD and 66 kD.
 Lane 6/7 - *N. meningitidis* - a protein of approximate weights of 13 kD, identified by reaction with Mab RV1.

FIGURE 12



1 2 3/4

Immunooblots of HIV1 antigens reacted with RV Mab RV1.
HTLV-IIIB viral lysate, lot #54-040, purchased from Applied
Biotechnologies, Inc., Md., USA.
Lane 1 - Molecular weight markers of 97, 66, 45, 31, 21, and 14 kD.
Lane 2 - Control RV antigens, 31 and 45 kD, reacting with RV1 Mab.
Lane 3/4 - HIV1 antigen of approximate weights of proteins at 24 kD
and 61 kD, identified by reaction with Mab RV1.

FIGURE 13